

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Motoharu SEIKI et al.
- (ii) TITLE OF INVENTION: NOVEL PROTEIN AND MONOCLONAL ANTIBODY SPECIFIC THERETO
- (iii) NUMBER OF SEQUENCES: 14
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
(B) STREET: 2033 K Street, N.W., Suite 800
(C) CITY: Washington
(D) STATE: D.C.
(E) COUNTRY: U.S.A.
(F) ZIP: 20006
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: MS-DOS
(D) SOFTWARE: Wordperfect 5.1
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: NEW
(B) FILING DATE: December 12, 2000
(C) CLASSIFICATION:
- (vi) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 09/000,041
(B) FILING DATE: February 20, 1998
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: PCT/JP96/01956
(B) FILING DATE: July 12, 1996
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Lee Cheng
(B) REGISTRATION NUMBER: 40,949
(C) REFERENCE/DOCKET NUMBER:
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 202-721-8200
(B) TELEFAX: 202-721-8250
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2116
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

09734003-121200

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GGCTCCTTAC CCACCCGGAG ACTTTTTTTTTT GAAAGGAAAC TAGGGAGGGAGGGAGAGGGA	60
GAGAGGGAGA AAACGAAGGG GAGCTCGTCC ATCCATTGAA GCACAGTTCA CT ATG	115
	Met
	1
ATC TTA CTC ACA TTC AGC ACT GGA AGA CGG TTG GAT TTC GTG CAT CAT	163
Ile Leu Leu Thr Phe Ser Thr Gly Arg Arg Leu Asp Phe Val His His	
	5 10 15
TCG GGG GTG TTT TTC TTG CAA ACC TTG CTT TGG ATT TTA TGT GCT ACA	211
Ser Gly Val Phe Phe Leu Gln Thr Leu Leu Trp Ile Leu Cys Ala Thr	
	20 25 30
GTC TGC GGA ACG GAG CAG TAT TTC AAT GTG GAG GTT TGG TTA CAA AAG	259
Val Cys Gly Thr Glu Gln Tyr Phe Asn Val Glu Val Trp Leu Gln Lys	
	35 40 45
TAC GGC TAC CTT CCA CCG ACT GAC CCC AGA ATG TCA GTG CTG CGC TCT	307
Tyr Gly Tyr Leu Pro Pro Thr Asp Pro Arg Met Ser Val Leu Arg Ser	
	50 55 60 65
GCA GAG ACC ATG CAG TCT GCC CTA GCT GCC ATG CAG CAG TTC TAT GGC	355
Ala Glu Thr Met Gln Ser Ala Leu Ala Ala Met Gln Gln Phe Tyr Gly	
	70 75 80
ATT AAC ATG ACA GGA AAA GTG GAC AGA AAC ACA ATT GAC TGG ATG AAG	403
Ile Asn Met Thr Gly Lys Val Asp Arg Asn Thr Ile Asp Trp Met Lys	
	85 90 95
AAG CCC CGA TGC GGT GTA CCT GAC CAG ACA AGA GGT AGC TCC AAA TTT	451
Lys Pro Arg Cys Gly Val Pro Asp Gln Thr Arg Gly Ser Ser Lys Phe	
	100 105 110
CAT ATT CGT CGA AAG CGA TAT GCA TTG ACA GGA CAG AAA TGG CAG CAC	499
His Ile Arg Arg Lys Arg Tyr Ala Leu Thr Gly Gln Lys Trp Gln His	
	115 120 125
AAG CAC ATC ACT TAC AGT ATA AAG AAC GTA ACT CCA AAA GTA GGA GAC	547
Lys His Ile Thr Tyr Ser Ile Lys Asn Val Thr Pro Lys Val Gly Asp	
	130 135 140 145
CCT GAG ACT CGT AAA GCT ATT CGC CGT GCC TTT GAT GTG TGG CAG AAT	595
Pro Glu Thr Arg Lys Ala Ile Arg Arg Ala Phe Asp Val Trp Gln Asn	
	150 155 160
GTA ACT CCT CTG ACA TTT GAA GAA GTT CCC TAC AGT GAA TTA GAA AAT	643
Val Thr Pro Leu Thr Phe Glu Glu Val Pro Tyr Ser Glu Leu Glu Asn	
	165 170 175

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GGC AAA CGT GAT GTG GAT ATA ACC ATT ATT TTT GCA TCT GGT TTC CAT	691
Gly Lys Arg Asp Val Asp Ile Thr Ile Ile Phe Ala Ser Gly Phe His	
180 185 190	
GGG GAC AGC TCT CCC TTT GAT GGA GAG GGA GGA TTT TTG GCA CAT GCC	739
Gly Asp Ser Ser Pro Phe Asp Gly Glu Gly Gly Phe Leu Ala His Ala	
195 200 205	
TAC TTC CCT GGA CCA GGA ATT GGA GGA GAT ACC CAT TTT GAC TCA GAT	787
Tyr Phe Pro Gly Pro Gly Ile Gly Gly Asp Thr His Phe Asp Ser Asp	
210 215 220 225	
GAG CCA TGG ACA CTA GGA AAT CCT AAT CAT GAT GGA AAT GAC TTA TTT	835
Glu Pro Trp Thr Leu Gly Asn Pro Asn His Asp Gly Asn Asp Leu Phe	
230 235 240	
CTT GTA GCA GTC CAT GAA CTG GGA CAT GCT CTG GGA TTG GAG CAT TCC	883
Leu Val Ala Val His Glu Leu Gly His Ala Leu Gly Leu Glu His Ser	
245 250 255	
AAT GAC CCC ACT GCC ATC ATG GCT CCA TTT TAC CAG TAC ATG GAA ACA	931
Asn Asp Pro Thr Ala Ile Met Ala Pro Phe Tyr Gln Tyr Met Glu Thr	
260 265 270	
GAC AAC TTC AAA CTA CCT AAT GAT GAT TTA CAG GGC ATC CAG AAA ATA	979
Asp Asn Phe Lys Leu Pro Asn Asp Asp Leu Gln Gly Ile Gln Lys Ile	
275 280 285	
TAT GGT CCA CCT GAC AAG ATT CCT CCA CCT ACA AGA CCT CTA CCG ACA	1027
Tyr Gly Pro Pro Asp Lys Ile Pro Pro Pro Thr Arg Pro Leu Pro Thr	
290 295 300 305	
GTG CCC CCA CAC CGC TCT ATT CCT CCG GCT GAC CCA AGG AAA AAT GAC	1075
Val Pro Pro His Arg Ser Ile Pro Pro Ala Asp Pro Arg Lys Asn Asp	
310 315 320	
AGG CCA AAA CCT CCT CGG CCT CCA ACC GGC AGA CCC TCC TAT CCC GGA	1123
Arg Pro Lys Pro Pro Arg Pro Pro Thr Gly Arg Pro Ser Tyr Pro Gly	
325 330 335	
GCC AAA CCC AAC ATC TGT GAT GGG AAC TTT AAC ACT CTA GCT ATT CTT	1171
Ala Lys Pro Asn Ile Cys Asp Gly Asn Phe Asn Thr Leu Ala Ile Leu	
340 345 350	
CGT CGT GAG ATG TTT GTT TTC AAG GAC CAG TGG TTT TGG CGA GTG AGA	1219
Arg Arg Glu Met Phe Val Phe Lys Asp Gln Trp Phe Trp Arg Val Arg	
355 360 365	
AAC AAC AGG GTG ATG GAT GGA TAC CCA ATG CAA ATT ACT TAC TTC TGG	1267
Asn Asn Arg Val Met Asp Gly Tyr Pro Met Gln Ile Thr Tyr Phe Trp	
370 375 380 385	
CGG GGC TTG CCT CCT AGT ATC GAT GCA GTT TAT GAA AAT AGC GAC GGG	1315
Arg Gly Leu Pro Pro Ser Ile Asp Ala Val Tyr Glu Asn Ser Asp Gly	
390 395 400	

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AAT TTT GTG TTC TTT AAA GGT AAC AAA TAT TGG GTG TTC AAG GAT ACA	1363
Asn Phe Val Phe Phe Lys Gly Asn Lys Tyr Trp Val Phe Lys Asp Thr	
405 410 415	
ACT CTT CAA CCT GGT TAC CCT CAT GAC TTG ATA ACC CTT GGA AGT GGA	1411
Thr Leu Gln Pro Gly Tyr Pro His Asp Leu Ile Thr Leu Gly Ser Gly	
420 425 430	
ATT CCC CCT CAT GGT ATT GAT TCA GCC ATT TGG TGG GAG GAC GTC GGG	1459
Ile Pro Pro His Gly Ile Asp Ser Ala Ile Trp Trp Glu Asp Val Gly	
435 440 445	
AAA ACC TAT TTC TTC AAG GGA GAC AGA TAT TGG AGA TAT AGT GAA GAA	1507
Lys Thr Tyr Phe Phe Lys Gly Asp Arg Tyr Trp Arg Tyr Ser Glu Glu	
450 455 460 465	
ATG AAA ACA ATG GAC CCT GGC TAT CCC AAG CCA ATC ACA GTC TGG AAA	1555
Met Lys Thr Met Asp Pro Gly Tyr Pro Lys Pro Ile Thr Val Trp Lys	
470 475 480	
GGG ATC CCT GAA TCT CCT CAG GGA GCA TTT GTA CAC AAA GAA AAT GGC	1603
Gly Ile Pro Glu Ser Pro Gln Gly Ala Phe Val His Lys Glu Asn Gly	
485 490 495	
TTT ACG TAT TTC TAC AAA GGA AAG GAG TAT TGG AAA TTC AAC AAC CAG	1651
Phe Thr Tyr Phe Tyr Lys Gly Lys Glu Tyr Trp Lys Phe Asn Asn Gln	
500 505 510	
ATA CTC AAG GTA GAA CCT GGA CAT CCA AGA TCC ATC CTC AAG GAT TTT	1699
Ile Leu Lys Val Glu Pro Gly His Pro Arg Ser Ile Leu Lys Asp Phe	
515 520 525	
ATG GGC TGT GAT GGA CCA ACA GAC AGA GTT AAA GAA GGA CAC AGC CCA	1747
Met Gly Cys Asp Gly Pro Thr Asp Arg Val Lys Glu Gly His Ser Pro	
530 535 540 545	
CCA GAT GAT GTA GAC ATT GTC ATC AAA CTG GAC AAC ACA GCC AGC ACT	1795
Pro Asp Asp Val Asp Ile Val Ile Lys Leu Asp Asn Thr Ala Ser Thr	
550 555 560	
GTG AAA GCC ATA GCT ATT GTC ATT CCC TGC ATC TTG GCC TTA TGC CTC	1843
Val Lys Ala Ile Ala Ile Val Ile Pro Cys Ile Leu Ala Leu Cys Leu	
565 570 575	
CTT GTA TTG GTT TAC ACT GTG TTC CAG TTC AAG AGG AAA GGA ACA CCC	1891
Leu Val Leu Val Tyr Thr Val Phe Gln Phe Lys Arg Lys Gly Thr Pro	
580 585 590	
CGC CAC ATA CTG TAC TGT AAA CGC TCT ATG CAA GAG TGG GTG TGATGTAGG	1942
Arg His Ile Leu Tyr Cys Lys Arg Ser Met Gln Glu Trp Val	
595 600 605	
GTTTTTCTT CTTTCTTTCT TTTGCAGGAG TTTGTGGTAA CTTGAGATTC AAGACAAGAG	2002
CTGTTATGCT GTTTCCTAGC TAGGAGCAGG CTTGTGGCAG CCTGATTCGG GGCTGACCTT	2062
TCAAACCAGA GGGTTGCTGG TCCTGCACAT GAGTGGAAAT ACACTCATGG GGAA	2116

09734006-121200

(i) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

[illegible]

210					215					220					
Asp 225	Glu	Pro	Trp	Thr	Leu 230	Gly	Asn	Pro	Asn	His 235	Asp	Gly	Asn	Asp	Leu 240
Phe	Leu	Val	Ala	Val 245	His	Glu	Leu	Gly	His 250	Ala	Leu	Gly	Leu	Glu 255	His
Ser	Asn	Asp	Pro 260	Thr	Ala	Ile	Met	Ala 265	Pro	Phe	Tyr	Gln	Tyr 270	Met	Glu
Thr	Asp	Asn 275	Phe	Lys	Leu	Pro	Asn 280	Asp	Asp	Leu	Gln	Gly 285	Ile	Gln	Lys
Ile	Tyr 290	Gly	Pro	Pro	Asp	Lys 295	Ile	Pro	Pro	Pro	Thr 300	Arg	Pro	Leu	Pro
Thr 305	Val	Pro	Pro	His	Arg 310	Ser	Ile	Pro	Pro	Ala 315	Asp	Pro	Arg	Lys	Asn 320
Asp	Arg	Pro	Lys	Pro 325	Pro	Arg	Pro	Pro	Thr 330	Gly	Arg	Pro	Ser	Tyr 335	Pro
Gly	Ala	Lys	Pro 340	Asn	Ile	Cys	Asp	Gly 345	Asn	Phe	Asn	Thr	Leu 350	Ala	Ile
Leu	Arg	Arg 355	Glu	Met	Phe	Val	Phe 360	Lys	Asp	Gln	Trp	Phe 365	Trp	Arg	Val
Arg	Asn 370	Asn	Arg	Val	Met	Asp 375	Gly	Tyr	Pro	Met	Gln 380	Ile	Thr	Tyr	Phe
Trp 375	Arg	Gly	Leu	Pro	Pro 390	Ser	Ile	Asp	Ala	Val 395	Tyr	Glu	Asn	Ser	Asp 400
Gly	Asn	Phe	Val	Phe 405	Phe	Lys	Gly	Asn	Lys 410	Tyr	Trp	Val	Phe	Lys 415	Asp
Thr	Thr	Leu 420	Gln	Pro	Gly	Tyr	Pro	His 425	Asp	Leu	Ile	Thr	Leu 430	Gly	Ser
Gly	Ile	Pro 435	Pro	His	Gly	Ile	Asp 440	Ser	Ala	Ile	Trp	Trp 445	Glu	Asp	Val
Gly	Lys 450	Thr	Tyr	Phe	Phe	Lys 455	Gly	Asp	Arg	Tyr	Trp 460	Arg	Tyr	Ser	Glu
Glu 465	Met	Lys	Thr	Met	Asp 470	Pro	Gly	Tyr	Pro	Lys 475	Pro	Ile	Thr	Val	Trp 480
Lys	Gly	Ile	Pro	Glu 485	Ser	Pro	Gln	Gly	Ala 490	Phe	Val	His	Lys	Glu 495	Asn
Gly	Phe	Thr	Tyr 500	Phe	Tyr	Lys	Gly	Lys 505	Glu	Tyr	Trp	Lys	Phe 510	Asn	Asn
Gln	Ile	Leu	Lys	Val	Glu	Pro	Gly	His	Pro	Arg	Ser	Ile	Leu	Lys	Asp

515	520	525
Phe Met Gly Cys Asp Gly Pro Thr Asp Arg Val Lys Glu Gly His Ser		
530	535	540
Pro Pro Asp Asp Val Asp Ile Val Ile Lys Leu Asp Asn Thr Ala Ser		
545	550	555
Thr Val Lys Ala Ile Ala Ile Val Ile Pro Cys Ile Leu Ala Leu Cys		
	565	570
Leu Leu Val Leu Val Tyr Thr Val Phe Gln Phe Lys Arg Lys Gly Thr		
	580	585
Pro Arg His Ile Leu Tyr Cys Lys Arg Ser Met Gln Glu Trp Val		
	595	600
		605

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

SGNVVNGCWG AYATMRTSAT

20

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

YTCRTSNTCR TCRAARTGRR HRTCYCC

27

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14
- (B) TYPE: Amino acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Gln Thr Arg Gly Ser Ser Lys Phe His Ile Arg Arg Lys Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14
(B) TYPE: Amino acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Glu Glu Val Pro Tyr Ser Glu Leu Glu Asn Gly Lys Arg Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18
(B) TYPE: Amino acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Pro Thr Ser Pro Arg Met Ser Val Val Arg Ser Ala Glu Thr Met Gln
1 5 10 15

Ser Ala

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14
(B) TYPE: Amino acid
(D) STRANDEDNESS: Single
(C) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Thr Leu Gly Asn Pro Asn His Asp Gly Asn Asp Leu Phe Leu
1 5 10

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(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7
(B) TYPE: Amino acid
(D) STRANDEDNESS: Single
(C) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Gly Glu Ala Asp Ile Leu Val
1 5

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9
(B) TYPE: Amino acid
(D) STRANDEDNESS: Single
(C) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Gly Asp Ala His Phe Asp Asp Asp Glu
1 5

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7
(B) TYPE: Amino acid
(D) STRANDEDNESS: Single
(C) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Gly Glu Ala Asp Ile Met Ile
1 5

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7
(B) TYPE: Amino acid
(D) STRANDEDNESS: Single
(C) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Pro Arg Cys Gly Val Pro Asp
1 5

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24
(B) TYPE: Amino Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

Ala Ile Ala Ile Val Ile Pro Cys Ile Leu Ala Leu Cys Leu Leu
1 5 10 15

Val Leu Val Tyr Thr Val Phe Gln Phe
20

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4
(B) TYPE: Amino Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Arg Xaa Lys Arg
1

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